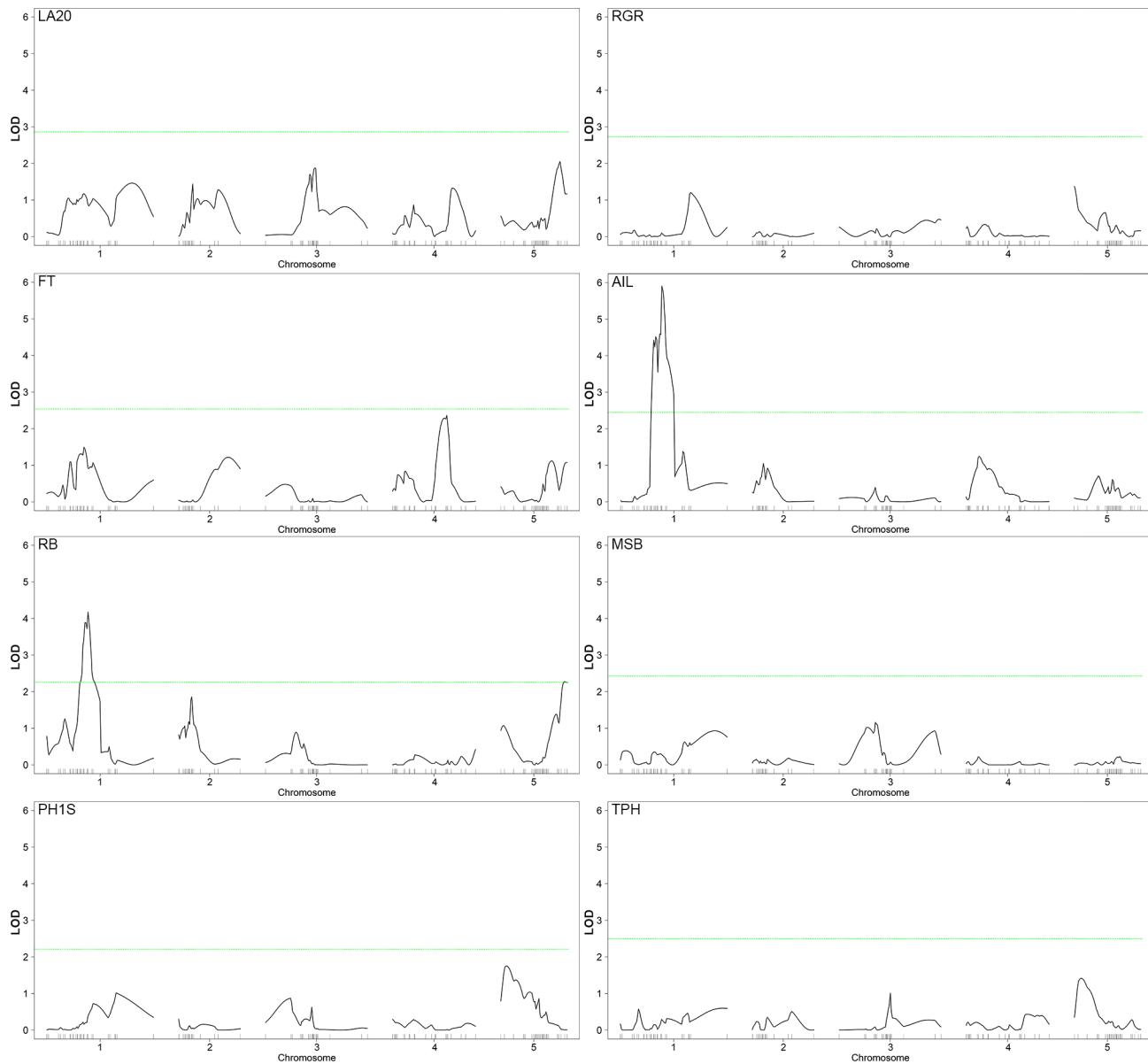
**Supplemental Figure 1.** Boxplots of epiRIL variation and phenotypic plasticity.

(A) Boxplots showing variation within epiRIL population.

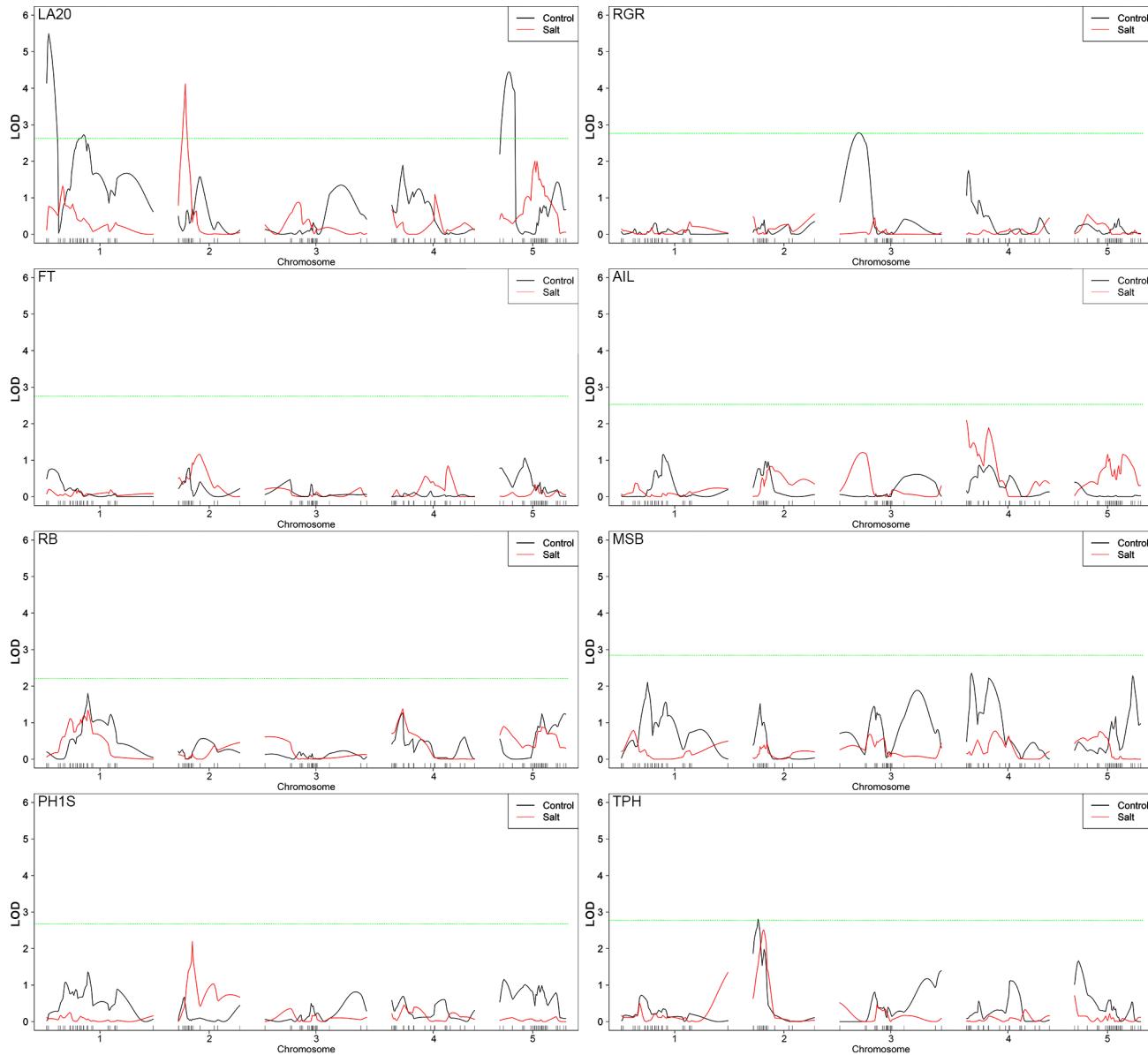
(B) Boxplots showing distribution of phenotypic plasticity for all epiRILs.

(C) Boxplots showing distribution of the coefficient of variation (CV) for the within-line variation for all epiRILs.

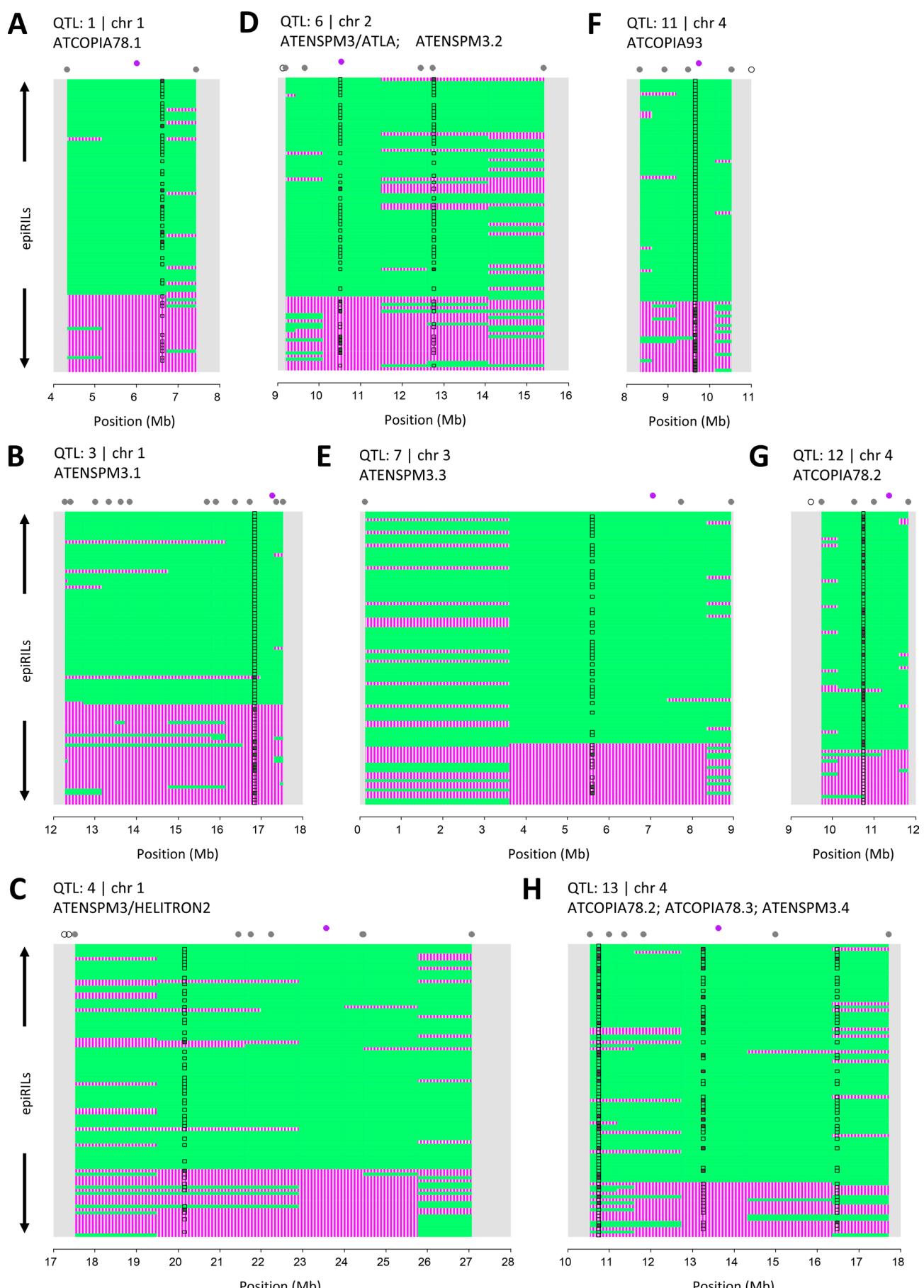
Boxplots showing variation within epiRIL population based on the minimum, first quartile, median, third quartile and maximum. The blue dot indicates the Col-0 parent value, the red dot indicates the *ddm1-2* parent value, the orange dot indicates the average value of all epiRILs and the black stars indicate suspected outliers (Tukey).Abbreviations used: LA20, leaf area after 20 days; RGR, relative growth rate; FT, flowering time; AIL, average internode length; RB, rosette branching; MSB, main stem branching; PH1S, plant height 1<sup>st</sup> silique; TPH, total plant height; C, control; S, saline.



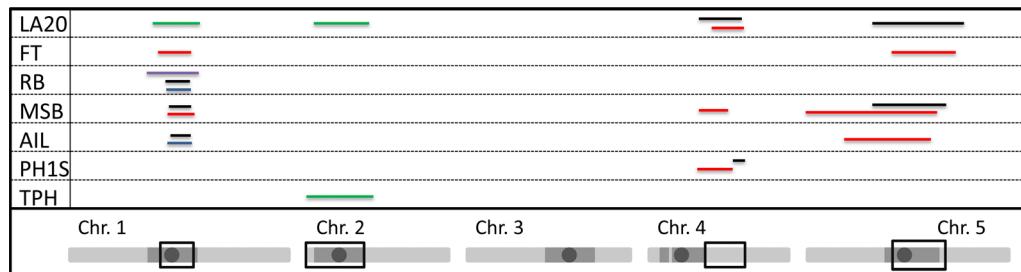
**Supplemental Figure 2.** Epi-QTL plots for phenotypic plasticity measured as the absolute difference in means between control and saline conditions. LOD threshold (horizontal green line) was calculated using 100 permutations with 0.05 as the genome-wide type I error level. Abbreviations used: LA20, leaf area after 20 days; RGR, relative growth rate; FT, flowering time; AIL, average internode length; RB, rosette branching; MSB, main stem branching; PH1S, plant height 1<sup>st</sup> silique; TPH, total plant height.



**Supplemental Figure 3.** Epi-QTL plots for coefficient of variation (CV) of the morphological traits tested in epiRIL population under control (black line) and saline (red line) conditions. LOD threshold (horizontal green line) was calculated using 100 permutations with 0.05 as the genome-wide type I error level. Abbreviations used: LA20, leaf area after 20 days; RGR, relative growth rate; FT, flowering time; AIL, average internode length; RB, rosette branching; MSB, main stem branching; PH1S, plant height 1<sup>st</sup> silique; TPH, total plant height.



**Supplemental Figure 4.** Locations of insertions inside QTL confidence intervals. Shown are the locations (black filled squares) of shared TE insertions inside the QTL confidence intervals; open squares indicate epiRILs for which no TE insertion was detected (PCR or sequencing); no square indicates epiRILs with no data for that TE. EpiRILs are ordered according to the epigenotype of the marker (top: WT, green; bottom: *ddm1-2*, red). Marker positions are indicated at the top (open dot: outside interval; grey dot: inside interval; purple dot: peak marker). (A-C): QTL 1, 3 and 4 on chr 1; (D): QTL 6 on chr 2; (E): QTL 7 on chr 3; (F-H): QTL 11 - 13 on chr 4. Other QTL intervals did not contain shared TE insertions.



**Supplemental Figure 5.** Overlap between QTLs found in our study and the validated epigenetic QTL for flowering time and root length in (Cortijo et al., 2014). Light grey bars indicate the five chromosomes of *Arabidopsis*, and the black box surrounding the chromosomes indicates the QTL intervals in (Cortijo et al., 2014). The colored lines indicate the QTL support intervals for the different traits in our study. Different colors indicate in which conditions the QTLs were found: black, neutral conditions; red, saline conditions; green, coefficient of variation (CV) in neutral conditions; purple, CV in saline conditions; blue, phenotypic plasticity (PP). Abbreviations used: LA20, leaf area after 20 days; FT, flowering time; RB, rosette branching; MSB, main stem branching; AIL, average internode length; PH1S, plant height 1<sup>st</sup> silique; TPH, total plant height.